Amendments to the Claims:

1. (Currently amended) A method to inactivate a ~~gene~~ nucleotide sequence of interest introduced into a genome of a plant cell, said method comprising:

transforming said plant cell with a nucleic acid molecule comprising a promoter operably linked to a said nucleotide sequence of interest ~~comprising said gene~~; and

introducing into said plant cell at least one chimeric oligonucleotide, said chimeric ~~oligonucleotide~~ oligonucleotide having at least a first block of RNA residues and a second block of RNA residues, wherein said first and said second blocks of RNA residues are homologous to said nucleic acid molecule and flank a block of DNA residues, wherein the block of DNA residues comprises at least one mismatch to the nucleic acid molecule and said chimeric oligonucleotide being capable of recognizing and implementing a nucleotide conversion in said nucleic acid molecule.

target molecule

2. (Originally filed) The method of claim 1, wherein said nucleotide conversion is in the promoter.

3. (Currently amended) The method of claim 1, wherein said nucleotide conversion is in a ~~the~~ coding region of said ~~gene~~ nucleotide sequence of interest.

4. (Currently amended) The method of claim 1, wherein said nucleotide sequence of interest ~~gene is~~ comprises a selectable a marker ~~gene~~.

5. (Currently amended) The method of claim 1, wherein said nucleotide sequence of interest ~~gene is a~~ modifies herbicide resistance ~~gene~~.

6. (Currently amended) The method of claim 1, wherein the chimeric oligonucleotide introduces a frameshift in the normal reading frame of the nucleotide sequence of interest ~~gene~~.

7. (Currently amended) The method of claim 1, wherein the chimeric oligonucleotide introduces a premature stop codon in the normal reading frame of the nucleotide sequence of interest ~~gene~~.

8. (Currently amended) The method of claim 2, wherein the chimeric oligonucleotide introduces a modification in a region of the promoter critical for transcription of the operably linked nucleotide sequence of interest ~~gene coding region~~.

9. (Currently amended) The method of claim 5, wherein said ~~herbicide resistance gene~~ nucleotide sequence of interest ~~is a~~ encodes 5-enol pyruvylshikimate-3-phosphate synthase ~~gene~~.

10. (Currently amended) The method of claim 5, wherein said ~~herbicide resistance~~ nucleotide sequence of interest ~~gene is an~~ encodes acetohydroxy acid synthetase ~~gene~~.

11. (Previously added) The method of claim 9, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10.

12. (Previously added) The method of claim 10, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 11, 12, and 13.

13. (Previously added) The method of claim 1, wherein said plant cell is from a monocot.

14. (Previously added) The method of claim 13, wherein said monocot is maize.

15. (Previously added) The method of claim 1, wherein said plant cell is from a dicot.

16. (Currently amended) A method to inactivate a ~~gene~~ nucleotide sequence of interest introduced into a genome of a plant, said method comprising:

transforming said plant with a nucleic acid molecule comprising a promoter operably linked to a said nucleotide sequence ~~comprising said gene~~;

introducing into said plant at least one chimeric oligonucleotide, said chimeric ~~oligonuleeotide~~ oligonucleotide having at least a first block of RNA residues and a second block of RNA residues, wherein said first and said second blocks of RNA residues are homologous to said nucleic acid molecule and flank a block of DNA residues, wherein the block of DNA residues comprises at least one mismatch to the nucleic acid molecule and said chimeric oligonucleotide being capable of recognizing and implementing a nucleotide conversion in said nucleic acid molecule.

17. (Previously added) The method of claim 16, wherein said nucleotide conversion is in the promoter.

18. (Currently amended) The method of claim 16, wherein said nucleotide conversion is in ~~the~~ a coding region of said nucleotide sequence of interest ~~gene~~.

19. (Currently amended) The method of claim 16, wherein the chimeric oligonucleotide introduces a frameshift in the normal reading frame of the nucleotide sequence of interest ~~gene~~.

20. (Currently amended) The method of claim 16, wherein the chimeric oligonucleotide introduces a premature stop codon in the normal reading frame of the nucleotide sequence of interest ~~gene~~.

21. (Currently amended) The method of claim 16, wherein said ~~gene~~ nucleotide sequence of interest ~~is a~~ comprises a selectable marker ~~gene~~.

22. (Currently amended) The method of claim 16, wherein said ~~gene~~ nucleotide sequence of interest ~~is a~~ modifies herbicide resistance ~~gene~~.

23. (Currently amended) The method of claim 22, wherein said ~~herbicide resistance gene~~ nucleotide sequence of interest encodes ~~is a~~ 5-enol pyruvylshikimate-3-phosphate synthase ~~gene~~.

24. (Currently amended) The method of claim 22, wherein said ~~herbicide resistance~~ nucleotide sequence of interest ~~gene is an~~ encodes acetohydroxy acid synthetase ~~gene~~.

C1

25. (Previously added) The method of claim 23, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10.

26. (Previously added) The method of claim 25, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 11, 12, and 13.

27. (Previously added) The method of claim 16, wherein said plant is a monocot.

28. (Previously added) The method of claim 27, wherein said monocot is maize.

29. (Previously added) The method of claim 16, wherein said plant is a dicot.